

**AMENDMENTS TO THE CLAIMS:**

Claims 1-22 are canceled without prejudice or disclaimer. Claims 23-34 are added. The following is the status of the claims of the above-captioned application, as amended.

Claims 1-22 (Canceled)

Claim 23 (New). A polypeptide having cellobiohydrolase II activity, selected from the group consisting of:

- (a) a polypeptide comprising an amino acid sequence selected from the group consisting of:
  - an amino acid sequence which has at least 75% identity with the amino acid sequence shown as amino acids 1 to 477 of SEQ ID NO:2,
  - an amino acid sequence which has at least 85% identity with the partial amino acid sequence shown as amino acids 1 to 82 of SEQ ID NO:4,
  - an amino acid sequence which has at least 85% identity with the amino acid sequence shown as amino acids 1 to 420 of SEQ ID NO:4,
  - an amino acid sequence which has at least 80% identity with the partial amino acid sequence shown as amino acids 1 to 139 of SEQ ID NO:6,
  - an amino acid sequence which has at least 95% identity with the partial amino acid sequence shown as amino acids 1 to 102 of SEQ ID NO:8,
  - an amino acid sequence which has at least 85% identity with the partial amino acid sequence shown as amino acids 1 to 144 of SEQ ID NO:10,
  - an amino acid sequence which has at least 75% identity with the partial amino acid sequence shown as amino acids 1 to 99 of SEQ ID NO:12,
  - an amino acid sequence which has at least 85% identity with the partial amino acid sequence shown as amino acids 1 to 140 of SEQ ID NO:14,
  - an amino acid sequence which has at least 75% identity with the partial amino acid sequence shown as amino acids 1 to 109 of SEQ ID NO:16,
  - an amino acid sequence which has at least 75% identity with the partial amino acid sequence shown as amino acids 1 to 407 of SEQ ID NO:16,

an amino acid sequence which has at least 75% identity with the partial amino acid sequence shown as amino acids 1 to 143 of SEQ ID NO:18,

an amino acid sequence which has at least 70% identity with the partial amino acid sequence shown as amino acids 1 to 71 of SEQ ID NO:20,

an amino acid sequence which has at least 60% identity with the amino acid sequence shown as amino acids 1 to 220 of SEQ ID NO:22,

an amino acid sequence which has at least 65% identity with the amino acid sequence shown as amino acids 1 to 458 of SEQ ID NO:24, and

an amino acid sequence which has at least 70% identity with the amino acid sequence shown as amino acids 1 to 390 of SEQ ID NO:26,

- (b) a polypeptide comprising an amino acid sequence selected from the group consisting of:  
an amino acid sequence which has at least 75% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Chaetomium thermophilum*,

an amino acid sequence which has at least 85% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Myceliophthora thermophila*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Melanocarpus albomyces*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Acremonium thermophilum*,

an amino acid sequence which has at least 95% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Melanocarpus* sp.,

an amino acid sequence which has at least 85% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Thielavia microspora*,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Aspergillus fumigatus*,

an amino acid sequence which has at least 75% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Aspergillus* sp.,

an amino acid sequence which has at least 85% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Thielavia australiensis*,

an amino acid sequence which has at least 75% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Aspergillus tubingensis*,

an amino acid sequence which has at least 75% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Gloeophyllum trabeum*,

an amino acid sequence which has at least 70% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Meripilus giganteus* ,

an amino acid sequence which has at least 60% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Trichophaea saccata* ,

an amino acid sequence which has at least 65% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Stilbella annulata*, and

an amino acid sequence which has at least 70% identity with the polypeptide encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in *Malbrancheae cinnamomea* .

- (c) a polypeptide comprising an amino acid sequence selected from the group consisting of:  
an amino acid sequence which has at least 75% identity with the polypeptide encoded by nucleotides 63 to 1493 of SEQ ID NO:1,

an amino acid sequence which has at least 85% identity with the polypeptide encoded by nucleotides 1 to 246 of SEQ ID NO:3,

an amino acid sequence which has at least 80% identity with the polypeptide encoded by nucleotides 1 to 417 of SEQ ID NO:5,

an amino acid sequence which has at least 95% identity with the polypeptide encoded by nucleotides 1 to 306 of SEQ ID NO:7,

an amino acid sequence which has at least 85% identity with the polypeptide encoded by nucleotides 1 to 432 of SEQ ID NO:9,

an amino acid sequence which has at least 75% identity with the polypeptide encoded by nucleotides 1 to 297 of SEQ ID NO:11,

an amino acid sequence which has at least 85% identity with the polypeptide encoded by nucleotides 1 to 420 of SEQ ID NO:13,

an amino acid sequence which has at least 75% identity with the polypeptide encoded by nucleotides 1 to 330 of SEQ ID NO:15,

an amino acid sequence which has at least 75% identity with the polypeptide encoded by nucleotides 1 to 1221 of SEQ ID NO:15,

an amino acid sequence which has at least 75% identity with the polypeptide encoded by nucleotides 1 to 429 of SEQ ID NO:17,

an amino acid sequence which has at least 70% identity with the polypeptide encoded by nucleotides 1 to 213 of SEQ ID NO:19,

an amino acid sequence which has at least 60% identity with the polypeptide encoded by nucleotides 43 to 701 of SEQ ID NO:21,

an amino acid sequence which has at least 65% identity with the polypeptide encoded by nucleotides 21 to 1394 of SEQ ID NO:23, and

an amino acid sequence which has at least 70% identity with the polypeptide encoded by nucleotides 41 to 1210 of SEQ ID NO:25,

(d) a polypeptide which is encoded by a nucleotide sequence which hybridizes under high stringency conditions with a polynucleotide probe selected from the group consisting of:

(i) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 63 to 1493 of SEQ ID NO:1,  
nucleotides 1 to 246 of SEQ ID NO:3,  
nucleotides 1 to 1272 of SEQ ID NO:3,  
nucleotides 1 to 417 of SEQ ID NO:5,  
nucleotides 1 to 306 of SEQ ID NO:7,  
nucleotides 1 to 432 of SEQ ID NO:9,  
nucleotides 1 to 297 of SEQ ID NO:11,  
nucleotides 1 to 420 of SEQ ID NO:13,  
nucleotides 1 to 330 of SEQ ID NO:15,  
nucleotides 1 to 1221 of SEQ ID NO:15,  
nucleotides 1 to 429 of SEQ ID NO:17,  
nucleotides 1 to 213 of SEQ ID NO:19,  
nucleotides 43 to 701 of SEQ ID NO:21,  
nucleotides 21 to 1394 of SEQ ID NO:23, and  
nucleotides 41 to 1210 of SEQ ID NO:25.

(ii) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 63 to 563 of SEQ ID NO:1,  
nucleotides 43 to 543 of SEQ ID NO:21,  
nucleotides 21 to 521 of SEQ ID NO:23, and  
nucleotides 41 to 541 of SEQ ID NO:25.

(iii) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 63 to 263 of SEQ ID NO:1,  
nucleotides 1 to 200 of SEQ ID NO:3,  
nucleotides 1 to 1272 of SEQ ID NO:3,  
nucleotides 1 to 200 of SEQ ID NO:5,  
nucleotides 1 to 200 of SEQ ID NO:5,  
nucleotides 1 to 200 of SEQ ID NO:7,  
nucleotides 1 to 200 of SEQ ID NO:9,

nucleotides 1 to 200 of SEQ ID NO:13,  
 nucleotides 1 to 200 of SEQ ID NO:11,  
 nucleotides 1 to 200 of SEQ ID NO:13,  
 nucleotides 1 to 200 of SEQ ID NO:15,  
 nucleotides 1 to 1221 of SEQ ID NO:15,  
 nucleotides 1 to 200 of SEQ ID NO:17,  
 nucleotides 1 to 200 of SEQ ID NO:19,  
 nucleotides 43 to 243 of SEQ ID NO:21,  
 nucleotides 21 to 221 of SEQ ID NO:23, and  
 nucleotides 41 to 241 of SEQ ID NO:25.

(e) a fragment of (a), (b) or (c) that has cellobiohydrolase II activity.

Claim 24 (New). The polypeptide according to claim 23, comprising an amino acid sequence selected from the group consisting of:

a polypeptide comprising an amino acid sequence selected from the group consisting of:  
 an amino acid sequence which has at least 80% identity with the amino acid sequence shown as amino acids 1 to 477 of SEQ ID NO:2,

an amino acid sequence which has at least 90% identity with the partial amino acid sequence shown as amino acids 1 to 82 of SEQ ID NO:4,

an amino acid sequence which has at least 90% identity with the amino acid sequence shown as amino acids 1 to 420 of SEQ ID NO:4,

an amino acid sequence which has at least 85% identity with the partial amino acid sequence shown as amino acids 1 to 156 of SEQ ID NO:6,

an amino acid sequence which has at least 80% identity with the partial amino acid sequence shown as amino acids 1 to 139 of SEQ ID NO:6,

an amino acid sequence which has at least 96% identity with the partial amino acid sequence shown as amino acids 1 to 102 of SEQ ID NO:8,

an amino acid sequence which has at 90% identity with the partial amino acid sequence shown as amino acids 1 to 144 of SEQ ID NO:10,

an amino acid sequence which has at least 80% identity with the partial amino acid sequence shown as amino acids 1 to 99 of SEQ ID NO:12,

an amino acid sequence which has at least 90% identity with the partial amino acid sequence shown as amino acids 1 to 140 of SEQ ID NO:14,

an amino acid sequence which has at least 80% identity with the partial amino acid sequence shown as amino acids 1 to 109 of SEQ ID NO:16,

an amino acid sequence which has at least 80% identity with the amino acid sequence shown as amino acids 1 to 407 of SEQ ID NO:16,

an amino acid sequence which has at least 80% identity with the partial amino acid sequence shown as amino acids 1 to 143 of SEQ ID NO:18,

an amino acid sequence which has at least 75% identity with the partial amino acid sequence shown as amino acids 1 to 71 of SEQ ID NO:20,

an amino acid sequence which has at least 60% identity with the partial amino acid sequence shown as amino acids 1 to 220 of SEQ ID NO:22,

an amino acid sequence which has at least 65% identity, with the amino acid sequence shown as amino acids 1 to 458 of SEQ ID NO:24, and

an amino acid sequence which has at least 75% identity with the amino acid sequence shown as amino acids 1 to 390 of SEQ ID NO:26.

Claim 25 (New). A polynucleotide having a nucleotide sequence which encodes for the polypeptide defined in claim 23.

Claim 26 (New). A nucleic acid construct comprising the nucleotide sequence defined in claim 25 operably linked to one or more control sequences that direct the production of the polypeptide in a suitable host.

Claim 27 (New). A recombinant expression vector comprising the nucleic acid construct defined in claim 26.

Claim 28 (New). A recombinant host cell comprising the nucleic acid construct defined in claim 26.

Claim 29 (New). A method for producing a polypeptide, the method comprising:

- (a) cultivating a recombinant host cell as defined in claim 28 under conditions conducive for production of the polypeptide; and
- (b) recovering the polypeptide.

Claim 30 (New). A polynucleotide comprising a nucleotide sequence which has at least 80% with a nucleotide selected from the group consisting of:

nucleotides 63 to 1493 of SEQ ID NO:1,  
nucleotides 1 to 246 of SEQ ID NO:3,  
nucleotides 1 to 1272 of SEQ ID NO:3,  
nucleotides 1 to 417 of SEQ ID NO:5,  
nucleotides 1 to 306 of SEQ ID NO:7,  
nucleotides 1 to 432 of SEQ ID NO:9,  
nucleotides 1 to 297 of SEQ ID NO:11,  
nucleotides 1 to 420 of SEQ ID NO:13,  
nucleotides 1 to 330 of SEQ ID NO:15,  
nucleotides 1 to 1221 of SEQ ID NO:15,  
nucleotides 1 to 429 of SEQ ID NO:17,  
nucleotides 1 to 213 of SEQ ID NO:19,  
nucleotides 43 to 701 of SEQ ID NO:21,  
nucleotides 21 to 1394 of SEQ ID NO:23, and  
nucleotides 41 to 1210 of SEQ ID NO:25.

Claim 31 (New). A polynucleotide having a nucleotide sequence which encodes a polypeptide having cellobiohydrolase II activity, and which hybridizes under high stringency conditions with a polynucleotide probe selected from the group consisting of:

- (i) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 63 to 1493 of SEQ ID NO:1,  
nucleotides 1 to 246 of SEQ ID NO:3,



nucleotides 1 to 1272 of SEQ ID NO:3,  
 nucleotides 1 to 417 of SEQ ID NO:5,  
 nucleotides 1 to 306 of SEQ ID NO:7,  
 nucleotides 1 to 432 of SEQ ID NO:9,  
 nucleotides 1 to 297 of SEQ ID NO:11,  
 nucleotides 1 to 420 of SEQ ID NO:13,  
 nucleotides 1 to 330 of SEQ ID NO:15,  
 nucleotides 1 to 1221 of SEQ ID NO:15,  
 nucleotides 1 to 429 of SEQ ID NO:17,  
 nucleotides 1 to 213 of SEQ ID NO:19,  
 nucleotides 43 to 701 of SEQ ID NO:21,  
 nucleotides 21 to 1394 of SEQ ID NO:23, and  
 nucleotides 41 to 1210 of SEQ ID NO:25.

(ii) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 63 to 563 of SEQ ID NO:1,  
 nucleotides 43 to 543 of SEQ ID NO:21,  
 nucleotides 21 to 521 of SEQ ID NO:23, and  
 nucleotides 41 to 541 of SEQ ID NO:25.

(iii) the complementary strand of the nucleotides selected from the group consisting of:

nucleotides 63 to 263 of SEQ ID NO:1,  
 nucleotides 1 to 200 of SEQ ID NO:3,  
 nucleotides 1 to 200 of SEQ ID NO:5,  
 nucleotides 1 to 200 of SEQ ID NO:7,  
 nucleotides 1 to 200 of SEQ ID NO:9,  
 nucleotides 1 to 200 of SEQ ID NO:11,  
 nucleotides 1 to 200 of SEQ ID NO:13,  
 nucleotides 1 to 200 of SEQ ID NO:15,  
 nucleotides 1 to 1221 of SEQ ID NO:15,  
 nucleotides 1 to 200 of SEQ ID NO:17,  
 nucleotides 1 to 200 of SEQ ID NO:19,  
 nucleotides 43 to 243 of SEQ ID NO:21,

nucleotides 21 to 221 of SEQ ID NO:23, and  
nucleotides 41 to 241 of SEQ ID NO:25.

Claim 32 (New). A polypeptide having cellobiohydrolase II activity which is encoded by the cellobiohydrolase II encoding part of the nucleotide sequence present in a microorganism selected from the group consisting of:

- a microorganism belonging to the family *Chaetomiaceae*, ,
- a microorganism belonging to the genus *Myceliophthora*, ,
- a microorganism belonging to the species *Acremonium thermophilum*,
- a microorganism belonging to the family *Chaetomiaceae*,
- a microorganism belonging to the genus *Aspergillus*,
- a microorganism belonging to the family *Chaetomiaceae*, p,
- a microorganism belonging to the genus *Aspergillus*,
- a microorganism belonging to the *Polyporales*,
- a microorganism belonging to the *Hymenochaetales*, pa microorganism belonging to the *Pezizomycotina*, a microorganism belonging to the species *Stilbella annulata*, and
- a microorganism belonging to the species *Malbranchea cinnamomea*.

Claim 33 (New). A transgenic plant, plant part or plant cell, which has been transformed with a nucleotide sequence encoding a polypeptide having cellobiohydrolase II activity as defined in claim 23.

Claim 34 (New). A detergent composition comprising a surfactant and the polypeptide according to claim 23.